

Figure 1

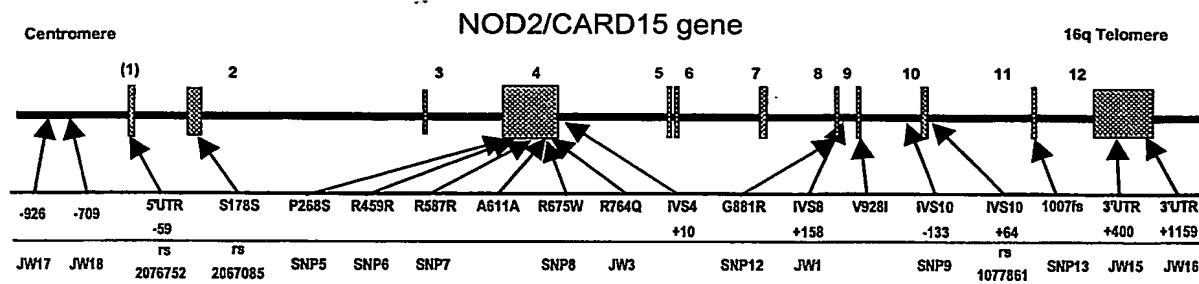


Figure 2

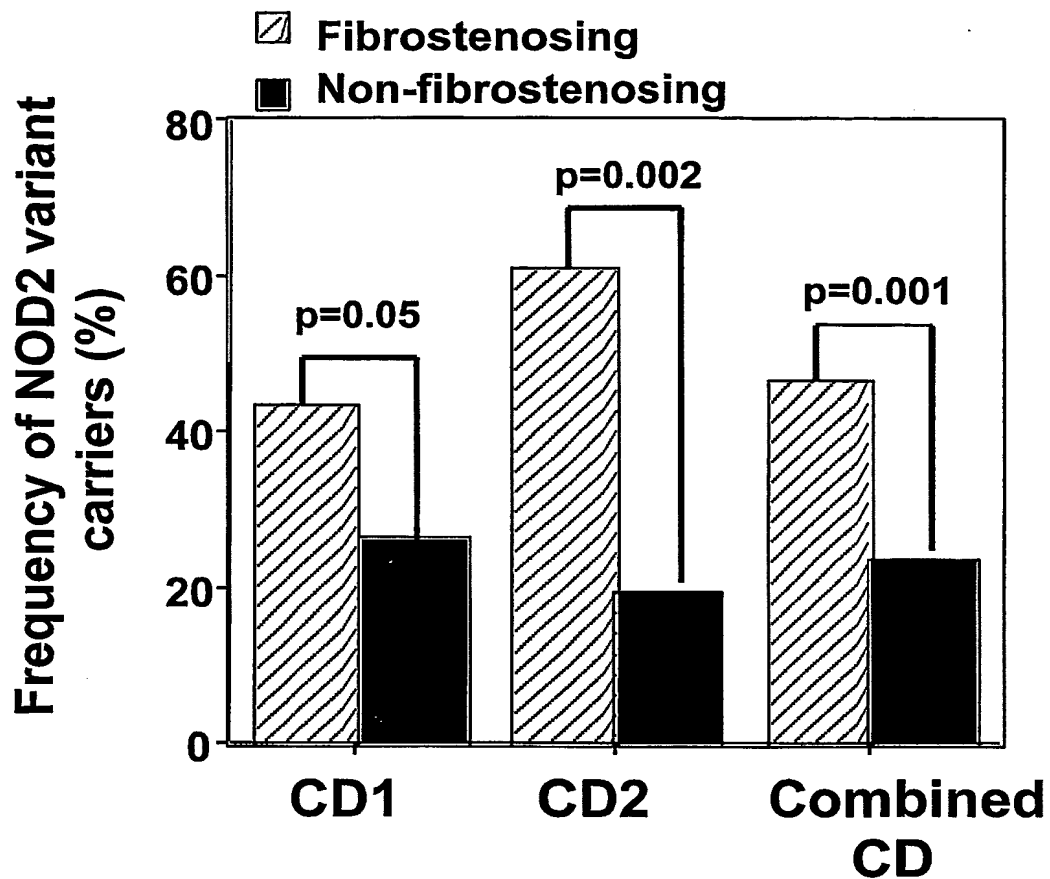


Figure 3

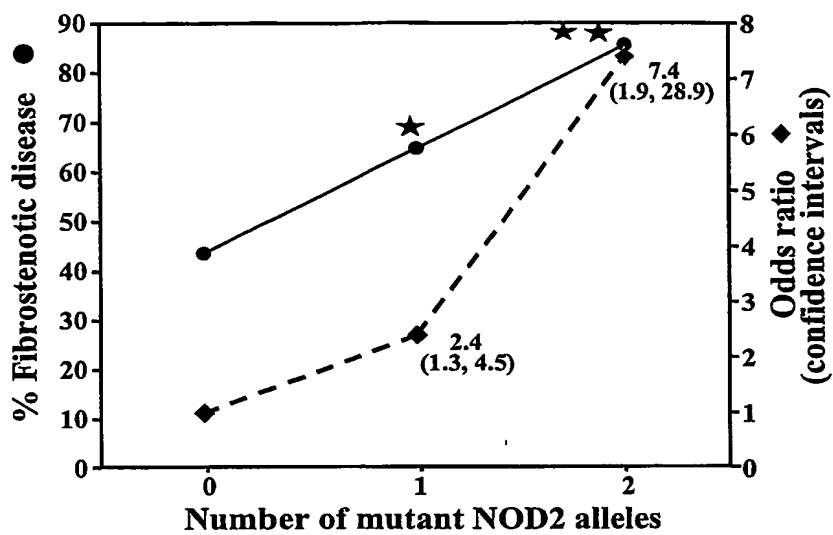
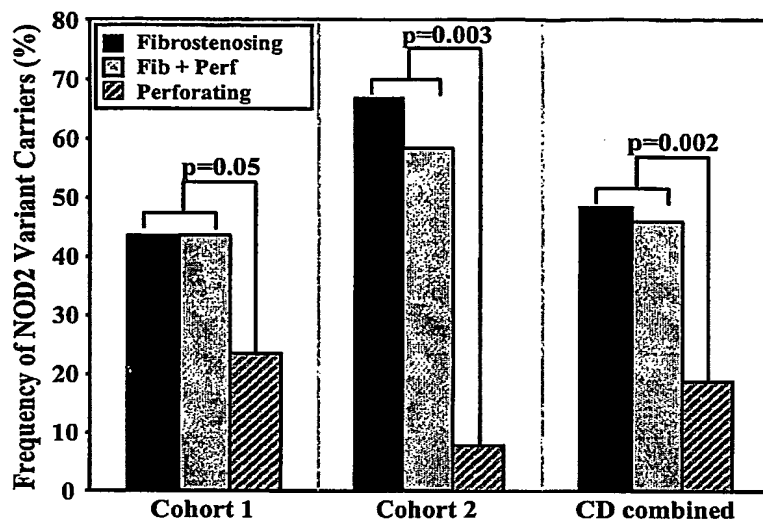


Figure 4



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FIGURE 5  
SNP 8

5' ACCCTTCAGT CACAGCGCC TTCTGCGC GGTGTGTG CCGGACAC 50  
 3' TGGAGTCTA GTCTGTCCG AAGCAAGTC CCGCTACAG GCGGCTGTG  
 TGGGCGCTCC TGGCTGAGTG CCGCTACTT CACAGCGCC TGGTCCGCTC 100  
 ACCCGGACG ACCACTCAC GTCTGTAGA CTCTTCGGG ACGAGGCGC  
 CCGCTGTG CCGGCTGGT GTCTGCGCG CAGGCTCCG AAGCTCTTC 150  
 GT CCGACAC GCGCGACCA CAGCTCGGC GTGGAGCGG TTCTGAGG  
 ACTCCATCC CCGCTTCA CCGGTGAGG CCGAGAGGT CATGCCATG 200  
 TCGGTAGCG CCGTCAAGT GCGCACTCC GGTCTTCCA CGTACGTAC  
 CCGGCTTCA TCTGCTCAT CCGGCGCTG TAGGATGTC AGGAGGAGG 250  
 GCGCCAACT AGCCGAGTA GCGTGGAC ATGCTCTAG TCTCTCTGC  
 CCGGCTTCC AAGCTGCAC GTGGCTGAA TGTGCGGC CCAAGTTCA 300  
 CCGCGACCC TTGGAGGTG CACCGACTT ACAACCGTG CAGTTCACT  
 CATTGTGCG TGTGCGGCG ACTGAGTGT CTGCGCTGG CTTTGTGCTG 350  
 GTAAACGTC ACGCGCGG TGTCTGCG CCGGGACCG CAACACGAC  
 CAGCACTTC GCGGCGCGT GCGGCTGCG CTGGCTTCA ACTCTGTGG 400  
 GTGTGAGCG CCGGCGCGA CCGGAGTTC GCGTCAATG TGAACACCC  
 TCACATGCG GTGGAGTAC TCTGCGTTC CCGTGTGTC TCGAGGCTC 450  
 ACTGTACCG CACCTGTTC AGGAGCAAC GCAACACAG ACCTTCTCG  
 TGTGTGAGT GTTACTCGG ATTCTGTTC AGGTATCGG CAGC 3' SEQ ID NO 1 494  
 ACATCACTCA CATGACCG TAAGTCAAG TCCATACCC CTCG 5' SEQ ID NO 2

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Figure 6

## SNP 12

5' ATCAAAACCC TGAGAGGACA AGGCACATTT CCAAGTCACC CAGAAAGACT 50  
 3' TAGTTTTGGG ACTCTCTGT TCCCTGTAAA GGTTCAGTGG GTCTTTCTGA  
  
 CGAGTGTCTT CTCTTGAAT CCAATGGTCT TTTTTCCTTA CTCCATTGCC 100  
 GCTCACAGGA GAGAACTTTA GGTACCAGA AAAAAGGAAT GAGGTAACGG  
  
 TAACATTGTG GGGTAGAAAT AAAGTTCAA GACCTTCAGA ACTGGCCCCA 150  
 ATTGTAACAC CCCATCTTTA TTTCAAGTTT CTGGAAGTCT TGACCGGGGT  
  
 GCTCTCCCT CTTCACCTGA TCTCCCCAAG AAAACTGCAG GATAGACTCT 200  
 CGAGGAGGGA GAAGTGGACT AGAGGGGTTC TTTTCACGTC CTATCTGAGA  
  
 GAAGCTTACC TGAGCCACCT CAAGCTCTGG TGATCAGCCA AGGCTTCAGC 250  
 CTTCGAATGG ACTCGGTGGA GTTCGAGACC ACTAGTGGGT TCGAAGTGG  
  
 CAGGGCTGG GCCCCCTGT CACCCActct gttgccccag aaTCTGAAAA 300  
 GTCCCGGACC CGGGCGAGCA GTGGGTgaga caacgggggtc ttAGACTTTT  
  
 GGCCAAAAGA GTCAACAGAC AGTGTACAGTG AGTACCTGAT ATGTGTTCTA 350  
 CCGGTTTTCT CAGTTGCTG TCACAGTCAC TCATGGACTA TACACAAGAT  
  
 GACATGAACT AACAGTCTTC CTCCCTCTGC AGTCCCAGCC AGAGGGGCAG 400  
 CTGTACTTGA TTGTACAGGAG GAGCGAGACG TCAGGGTGGG TCTCCCCGTC  
  
 GACCACTCAA TCCCAGAGTG GCCTCACTGG GGCTCTGGT OCCAGCAAAG 450  
 CTGGTGAGTT AGGGTCTCAC CGCAGTGACC CCGAGGACCA GGGTCGTTTC  
  
 TGGACCTGCC TCCATCTTTT GGGTGGGATG GCCAAACTTA ACCCAAGAGT 500  
 ACGTGAAGG AGGTAGAAAA CCCACCCTAC CCGTTTGAAT TGGGTCTCTA  
  
 TTTTCAGTGGC TTTACATTAC AGACTTAGAG AATAGTAGAG 3'-SEQ ID NO 3 540  
 AAAGTCACCG AAATGTAATG TCTGAATCTC TTATCATCTC 5'-SEQ ID NO 4

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FIGURE 7

## SNP 13

5' TTTAAAAATG AATCATTGC TCCCTACTTA AACAGGTAAA CACTTCTTTC 50  
 3' AAATTTTTC TTTAGTAACG AGGGATGAAT TTCTCCATTT CTGAAGAAAG  
  
 TTACACAGAG AATCAGATCC TTCACATGCA GAATCATTCT CACTGAATGT 100  
 AATCTGTCTC TTAGTCTAGG AAGTGTACGT CTTAGTAACA GTGACTTACA  
  
 CAGAATCAGA AGGGATCCTC AAAATTCTGC CATTCCTCTC TCCCGTCACC 150  
 GICTTAGTCT TCCCTAGGAG TTTTAAGACG GTAAGGACAG AGGCCAGTGC  
  
 CCATTTTACA CATAGAAAAA CTGAGGTTCG GAGAGCTAAA ACAGGCCTGC 200  
 GGTAAAAATGT CTATCTTTTT GACTCCAACC CTCCTGATTT TGTCGGGACG  
  
 CCAGGGCCT TACCAGACTT CCAGGATGGT GTCATT cctt tcaagggggcc 250  
 GGTCCTCCGA ATGGTCTGAA GGTCCTACCA CAGTAAggaa agttccccgg  
  
 tgc AGGAGCG CTCTCTGCCC TAGGTAGGIG ATGCAGTTAT TGGACAACCT 300  
 acg/TCCCTCC GAAGACGGGG ATCCATCCAC TACGTCAATA ACCTGTTGGA  
  
 GGAAAAGAAG ATACAATGGT GAGCTTCAAG GATTCTTGGT TTCTCTCTTG 350  
 CCTTTTCTTC TATGTTACCA CTCGAAGTTC CTAAGAACCA AAAGGAGAAC  
  
 AAACGTGTCA GTTAAAGAGA CTGCAGGAGT TAGCCAGTCT ACTGAAGCCC 400  
 TTTGACAGGT CAATTTCTCT GAGTCTCTCA ATCGGTGAGA TGAATTGGG  
  
 ACCTGTCCCT TAGACACATC CTGCTCATGT CTGAGATTCC CAATGAGCTC 450  
 TGGACAGCGA ATCTGTGTAG GACGAGTACA GACTCTAAGG GTTACTCGAG  
  
 ATCAACAAAG GCTCAGTACC ATCAGTGAAA TGTAACCGTC TCTCTTCCAT 500  
 TAGTTGTTTC CCAGTCATGG TAGTCACTTT ACATTGGCAG AGACAAGGTA  
  
 TCACTACATG AGTTTATCAA ATTAAGTAGC CACTCCCTTA G3'-SEQ ID NO 5 541  
 AGTGATCTAC TCAATAGTT TAATTCATCG GTGAGGGAAT C5'-SEQ ID NO 6

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FIGURE 8

SNP 5

5' AACAGCAGTG CTCAAAGAGT ACAGTCCGCA CAGCAGGTGG TTTCGCCATC 50  
 3' TTGTCGTAC GAGTTTCTCA TCTCAGCCGT GTCTCTCACC AAACCGGTAC  
  
 CACTGCAGCT GCGCGCAGCT GAATGGGAAG ACAAGAGAGAA ATTCTGCGAA 100  
 GTGACGTCCA CGGCGGTCCA CTTCACCTTC TGTTTCTCTT TAAGCACTTT  
  
 GTCTTGGCCCT GCAGCCCAACA GCAAGTGCAG CCGCTGCAGG AGCGTGGCTCT 150  
 CAGAAGCGGA CGTCGGGTGT CGTTCACGTC GCGCAGGTCC TCGCAGCAGA  
  
 TGCCACTGCC CGCTCAACC ACCACCAGCA CAGTGTCCGC ATCGTCAATTG 200  
 ACGGTCAACG GCGGAGTGGG TGGTGGTGGT GTACACGGCG TAGCAGTAAC  
  
 AGGTGGCAG GGGTGTGAA CAGCTCTCC AGGCCAGGG TGGCTGGGCT 250  
 TCCACCGGTC CCCACGACTT CTCCAGGAGG TCCGGTCCC ACCGACCGCA  
  
 CTCTGGGGT ggtccagcca tgccacatc TCCCCAGACC TCCAGGACAT 300  
 CAGACGGCC cgaggtcgt acgggtgtag ACCGGTCTGG AGGTCTGTG  
  
 TCTCTGTGTA TATGTCTCC AGGCAGACCG TCTCTGCTCC ATCATAGGTA 350  
 AGACACACAT ATACAGGAGG TCCGTCTCC AGACAGAGG TAGTATCCAT  
  
 CAGAGGAAGC GAGACTGAGC AGACACCGTG GTCTCAGCT TGGCCATATA 400  
 CACTCTTCG CTCTGACTCG TCTGTGGCAC CAGGAGTCCA ACCGGTATAT  
  
 CTCTTTCAT GTGGCAGCTG GAAGGCAGAA GAACAGCCAG ATGAAGGTGG 450  
 CAGAACGTA CACCGTCAC CTTCGGTCTT CTCTCCGTC TACTTCACC  
  
 CACCATGGTG APCACGGAC CTAACCAGAC AATGGGCTGC TCGCGGGAC 500  
 GTGGTACCAC TTCTGCGCTG GATGGTCTG TTACCGAGC AGGCCCCCTG  
  
 GCTGACATAA CTCAGGGAT AGCAGGCA GCGGCGGCG3'-SEQ ID NO 7 540  
 CGACTGTATT CACTTCCCTA TCTCTCGGT CGGCGCGGG5'-SEQ ID NO 8

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FIGURE 9

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5' CCAC TGGGCA CCCACTACCA ATCGATTGCA ATTGGTCCTT AACATAAAAT 50  
 3' CGTGACCCGT GGGTCATCGT TACCTAACCT TAACCAGGAA TTCTATTTTA  
  
 GTACCTGATC CAGCCCAATA TCTTCAATTT ACAGATACTG TATCAAAACC 100  
 CATGGACTAG GTGGGTTAT AGAAGTTAAA TGTCTATGAC ATAGTTTTGG  
  
 CTGAGAGGAC AAGGGACATT TOCAAGTAC CCAGT agac tggagtgtcc 150  
 GACTCTCTG TTCCCTGTAA AGGTTGAGTG GGTCttctg agctcacagg  
  
TCTCTTGA TCCAATGGTC TTTTTTCTT ACTCCATTGC CTAACATTGT 200  
ACAGACTTT AGGTTACCAG AAAAAAGGAA TGAGGTAAAG GATTGTAAAC  
  
 GGGGTAGAAA TAAAGTTCAA AGACCTTCAG AACTGGCCCC AGCTCTCTCC 250  
 CCCATCTTT ATTTCAAGTT TCTGGAAGTC TTGACCGGGG TCGAGCAGGG  
  
 TCTTCACCTG ATCTCCCCAA GAAACTGCA GGATAGACTC TGAAGCTTAC 300  
 AGAAGTGCAC TAGAGGGGTT CTTTGTAGCT CCTATCTGAG ACTTGAATG  
  
 CTGAGCCACC TCAAGCTCTG GTGATCAACC AAGCCTTCAG CCAGGGCCTG 350  
 GACTCGGTGG AGTTCCAGAC CACTAGTGGG TTCCCAAGTC GGTCCTCGAC  
  
 GGCCCCCTCG TCACCCACTC TGTTCGCCCCA GAATCTGAAA AGGCCAAAAG 400  
 CCGGGGGACC AGTGGGTGAG ACAACGGGGT CTTAGACTTT TCGGTTTTTC  
  
 AGTCAACAGA CAGTGTGAGT GAGTACCTGA TATGTGTCTT AGACATGAAC 450  
 TCAGTTGTCT GTACAGTCA CTCATGGACT ATACACAAGA TCTGTACTTG  
  
 TAACAGTCTT CTTCCCTCTG CAGTCCCACC CAGAGGGGCA GGACCACTCA 500  
 ATTGTACGA GAGGGCAGAC GTCAGGGTCG GTCTCCCCGT CCTGGTCACT  
  
 ATCCCAGAGT GGCTCACTG 3'-SEQ ID NO 9 520  
 TAGGGTCTCA CCGAGTGAC 5'-SEQ ID NO 10

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DNA ID	DNA ID
100	100
61	61
53	53
56	56
56	56
56	56
52	52
51	51
49	49
50	50
53	53
53	53

[illegible]

201	0008TD	AGCTATCTGCAATGCCCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	300
162	0101S87	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	261
154	02887	AGCTATCTGCAATGCCCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	253
157	03886	AGCTATCTGCAATGCCCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	256
157	04887	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	256
157	05887	AGCTATCTGCAATGCCCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	256
157	06882	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	256
153	08887	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	252
152	12887	AGCTATCTGCAATGCCCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	251
150	13887	AGCTATCTGCAATGCCCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	249
151	14887	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	250
154	19887	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	253
154	22887	AGCTATCTGCATTTGCGCTTTTGATCTCTACTTTCAGTTACTCAACAACCTTCAAAGACACCATTTGCTTCCCTCCAAAGGTGAGGCCCATGTGAGAAAAGGATCACT	253

FIGURE 10

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009TD	301	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	353	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
018S7	262	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	400	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
028S7	254	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	361	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
038S6	257	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	353	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
048S7	257	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	356	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
058S7	257	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	356	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
068S2	257	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	356	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
088S7	253	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	356	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
128S7	252	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	352	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
138S7	250	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	351	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
148S7	251	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	349	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
198S7	254	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	350	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
228S7	254	TCCTTGCTGAAAGAGAGGGGTCAAGGGG	353	TCCTTGCTGAAAGAGAGGGGTCAAGGGG
009TD	401	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	500	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
018S7	362	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	461	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
028S7	354	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	453	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
038S6	357	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	456	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
048S7	357	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	456	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
058S7	357	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	456	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
068S2	357	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	456	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
088S7	353	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	456	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
128S7	352	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	452	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
138S7	350	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	451	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
148S7	351	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	449	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
198S7	354	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	450	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
228S7	354	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG	453	AGCCAGCCCGGTTTCTCTGGGGCCAAAGAGG
009TD	501	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	535	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
018S7	462	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	496	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
028S7	454	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	488	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
038S6	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	491	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
048S7	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	491	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
058S7	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	491	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
068S2	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	491	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
088S7	453	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	487	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
128S7	452	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	486	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
138S7	450	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	484	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
148S7	451	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	485	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
198S7	454	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	488	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG
228S7	454	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG	488	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTG

FIGURE 10 (continued)

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SEQ ID NO:24	00STD	1	TCACATGCTCTGGTTCATGCTGTAACCTGCTGCAACACAGACCTCTGTAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	100
SEQ ID NO:25	01SS6	1	-----TGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:26	02SS6	1	-----TCCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	65
SEQ ID NO:27	03SS6	1	-----GACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	62
SEQ ID NO:28	04SS6	1	-----TGAACTCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	70
SEQ ID NO:29	05SS6	1	-----TGAACTCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	70
SEQ ID NO:30	06SS6	1	-----TGAACTCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	69
SEQ ID NO:31	08SS6	1	-----GAACTCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	69
SEQ ID NO:32	12SS6	1	-----TGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:33	13SS6	1	-----TGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:34	14SS6	1	-----TGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:35	19SS6	1	-----TCCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	65
SEQ ID NO:36	22SS6	1	-----CTCTGACACACAGACCTCTGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	66
00STD		101	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	200
01SS6		64	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	163
02SS6		66	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	165
03SS6		63	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	162
04SS6		71	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	170
05SS6		71	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	170
06SS6		70	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	169
08SS6		70	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	169
12SS6		64	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	163
13SS6		71	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	170
14SS6		64	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	163
19SS6		66	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	165
22SS6		67	TTAGGATGTACAGTTATGGAATGCAAGATTTACAGGAATTTAGGCGCTTCCTTCAAGACCAATGCTCTCTGGATTAATCAAAATGATGTATGTTG	166
00STD		201	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	300
01SS6		164	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	263
02SS6		166	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	265
03SS6		163	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	262
04SS6		171	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	270
05SS6		171	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	270
06SS6		170	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	269
08SS6		170	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	269
12SS6		164	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	263
13SS6		171	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	270
14SS6		164	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	263
19SS6		166	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	265
22SS6		167	AAGCCTTTGTAAATGTGCAGATGCTGCAAAATGTTATTTTAAACATTAATGATGTGAAACTGCTTAATATTTADAGCTTCACCTTTGTTTACTGT	266

JW16

FIGURE 11A

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DNA ID	301	CTTAAAGTTTATACCTCTTATAGACAA	301	CTTAAAGTTTATACCTCTTATAGACAA
009TD	264	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
01886	264	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
02886	266	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
03886	263	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
04886	271	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
05882	271	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
06886	270	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
08886	270	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
12886	264	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
13886	271	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
14886	264	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
19886	266	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
22886	267	CATGSCCGTGAACTTTATGCTGTAAATA	301	CTTAAAGTTTATACCTCTTATAGACAA
009TD	401	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
01886	364	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
02886	366	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
03886	363	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
04886	371	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
05882	371	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
06886	370	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
08886	370	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
12886	364	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
13886	371	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
14886	364	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
19886	366	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG
22886	367	ACCAACATTTTAAAAATATCTGCTGGG	401	ACCAACATTTTAAAAATATCTGCTGGG

FIGURE 11A (continued)

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SEQ ID NO:55	00STD	1	TTGGCTCTCAGTTTCTTTGTGACAGAGCTGTGAGTTT	100
SEQ ID NO:56	01896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	101
SEQ ID NO:57	02886	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	102
SEQ ID NO:58	03896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	103
SEQ ID NO:59	04886	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	104
SEQ ID NO:60	05896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	105
SEQ ID NO:61	06896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	106
SEQ ID NO:62	08896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	107
SEQ ID NO:63	12896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	108
SEQ ID NO:64	13896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	109
SEQ ID NO:65	14896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	110
SEQ ID NO:66	19896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	111
SEQ ID NO:67	22896	1	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	112
SEQ ID NO:68	00STD	101	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	113
SEQ ID NO:69	01896	65	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	114
SEQ ID NO:70	02886	65	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	115
SEQ ID NO:71	03896	65	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	116
SEQ ID NO:72	04896	51	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	117
SEQ ID NO:73	05896	68	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	118
SEQ ID NO:74	06896	67	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	119
SEQ ID NO:75	08896	66	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	120
SEQ ID NO:76	12896	66	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	121
SEQ ID NO:77	13896	66	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	122
SEQ ID NO:78	14896	71	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	123
SEQ ID NO:79	19896	21	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	124
SEQ ID NO:80	22896	68	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	125
SEQ ID NO:81	00STD	201	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	126
SEQ ID NO:82	01896	165	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	127
SEQ ID NO:83	02896	165	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	128
SEQ ID NO:84	03896	165	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	129
SEQ ID NO:85	04896	151	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	130
SEQ ID NO:86	05896	167	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	131
SEQ ID NO:87	06896	167	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	132
SEQ ID NO:88	08896	166	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	133
SEQ ID NO:89	12896	166	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	134
SEQ ID NO:90	13896	166	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	135
SEQ ID NO:91	14896	171	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	136
SEQ ID NO:92	19896	121	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	137
SEQ ID NO:93	22896	168	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	138
SEQ ID NO:94	00STD	300	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	139
SEQ ID NO:95	01896	165	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	140
SEQ ID NO:96	02896	165	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	141
SEQ ID NO:97	03896	165	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	142
SEQ ID NO:98	04896	151	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	143
SEQ ID NO:99	05896	167	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	144
SEQ ID NO:100	06896	167	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	145
SEQ ID NO:101	08896	166	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	146
SEQ ID NO:102	12896	166	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	147
SEQ ID NO:103	13896	166	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	148
SEQ ID NO:104	14896	171	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	149
SEQ ID NO:105	19896	121	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	150
SEQ ID NO:106	22896	168	-----GGGCCCCCAGAGGCTGGGTGACATGCTTGGCAGCCTCTTCAAAATGAGCCCTGCTTCCCTAAG	151

FIGURE 11B

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DNA ID	301	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	400	CCACTGCTCTGATGAAGAG
009TD	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	364	CCACTGCTCTGATGAAGAG
01886	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	364	CCACTGCTCTGATGAAGAG
02886	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	364	CCACTGCTCTGATGAAGAG
03886	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	364	CCACTGCTCTGATGAAGAG
04886	251	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	350	CCACTGCTCTGATGAAGAG
05886	268	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	367	CCACTGCTCTGATGAAGAG
06886	267	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	366	CCACTGCTCTGATGAAGAG
08886	266	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	365	CCACTGCTCTGATGAAGAG
12886	266	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	365	CCACTGCTCTGATGAAGAG
13886	266	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	365	CCACTGCTCTGATGAAGAG
14886	271	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	370	CCACTGCTCTGATGAAGAG
19886	221	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	320	CCACTGCTCTGATGAAGAG
22886	268	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTT	367	CCACTGCTCTGATGAAGAG
009TD	401	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	500	
01886	365	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	464	
02886	365	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	464	
03886	365	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	464	
04886	351	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	450	
05886	368	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	467	
06886	367	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	466	
08886	366	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	465	
12886	366	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	465	
13886	366	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	465	
14886	371	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	470	
19886	321	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	420	
22886	368	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCTCTGGACT	467	
008TD	501	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	533	
01886	465	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	497	
02886	465	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	497	
03886	465	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	497	
04886	451	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	483	
05886	468	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	500	
06886	467	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	499	
08886	466	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	498	
12886	466	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	498	
13886	466	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	498	
14886	471	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	503	
19886	421	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	453	
22886	468	CTTGACACAGCTCTCTCTCTGAGGCTGAAATT	500	

FIGURE 11B (continued)

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